



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 98211

TO: Juliet Switzer
Location: o 12D15; m 12E12
Art Unit: 1634
Monday, July 07, 2003

Case Serial Number: 09/326285

From: Barb O'Bryen
Location: Biotech-Chem Library
CM1-6A05
Phone: 308-4291

barbara.obryen@uspto.gov

Search Notes

O'Bryen, Barbara

From: Switzer, Juliet
Sent: Monday, June 30, 2003 11:56 AM
To: O'Bryen, Barbara
Subject: RE: search request 09/326285

Please modify search request as follows
Please search the following

seq id no 1 and the nucleic acid encoding seq id 9 in ALL nucleic acid databases

oligomer search for 500 nucleotides or more of sid 1 or 9 in all nucleic acid databases except interference

search seq id no 38-40 and 42-49 in interference databases only.

please return results on disk.

thanks.



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OM nucleic - nucleic search, using sw model

Run on: July 3, 2003, 12:13:11 ; Search time 34.9362 Seconds
(without alignments)
7645.798 Million cell updates/sec

Title: US-09-326-285-39
Perfect score: 871
Sequence: 1 tgattgactatctcattcct.....ctcactcgtagtcgtagctc 871

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	859	98.6	3153	4	US-09-080-625-3	Sequence 3, Appli
2	859	98.6	3153	4	US-09-695-782-3	Sequence 3, Appli
3	859	98.6	3336	4	US-09-080-625-2	Sequence 2, Appli
4	859	98.6	3336	4	US-09-695-782-2	Sequence 2, Appli
5	859	98.6	3694	4	US-09-080-625-5	Sequence 5, Appli
6	859	98.6	3694	4	US-09-695-782-5	Sequence 5, Appli
7	859	98.6	3877	4	US-09-080-625-4	Sequence 4, Appli
8	859	98.6	3877	4	US-09-695-782-4	Sequence 4, Appli

1 indel
1 gap
ceo?

OM nucleic - nucleic search, using sw model

Run on: July 3, 2003, 12:13:11 ; Search time 21.8602 Seconds
 (without alignments)
 7645.798 Million cell updates/sec

Title: US-09-326-285-40
 Perfect score: 545
 Sequence: 1 atcctcttcggagaagagag.....ctcactcgtagtcgtagctc 545

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_NA:*
 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	545	100.0	3153	4	US-09-080-625-3	Sequence 3, Appli
2	545	100.0	3153	4	US-09-695-782-3	Sequence 3, Appli
3	545	100.0	3336	4	US-09-080-625-2	Sequence 2, Appli
4	545	100.0	3336	4	US-09-695-782-2	Sequence 2, Appli
5	545	100.0	3694	4	US-09-080-625-5	Sequence 5, Appli
6	545	100.0	3694	4	US-09-695-782-5	Sequence 5, Appli
7	545	100.0	3877	4	US-09-080-625-4	Sequence 4, Appli
8	545	100.0	3877	4	US-09-695-782-4	Sequence 4, Appli
c 9	39.4	7.2	4488	4	US-08-406-030A-3	Sequence 3, Appli

OM nucleic - nucleic search, using sw model

Run on: July 3, 2003, 12:13:11 ; Search time 30.2032 Seconds
(without alignments)
7645.798 Million cell updates/sec

Title: US-09-326-285-44
Perfect score: 753
Sequence: 1 tgattgactatctcattcct.....ggtgtcgcgctgccccgac 753

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	741	98.4	3153	4	US-09-080-625-3	Sequence 3, Appli
2	741	98.4	3153	4	US-09-695-782-3	Sequence 3, Appli
3	741	98.4	3336	4	US-09-080-625-2	Sequence 2, Appli
4	741	98.4	3336	4	US-09-695-782-2	Sequence 2, Appli
5	741	98.4	3694	4	US-09-080-625-5	Sequence 5, Appli
6	741	98.4	3694	4	US-09-695-782-5	Sequence 5, Appli
7	741	98.4	3877	4	US-09-080-625-4	Sequence 4, Appli
8	741	98.4	3877	4	US-09-695-782-4	Sequence 4, Appli
9	40	5.3	3645	2	US-08-663-112-1	Sequence 1, Appli

one bp off
ceo?

OM nucleic - nucleic search, using sw model

Run on: July 3, 2003, 12:13:11 ; Search time 17.1272 Seconds
(without alignments)
7645.798 Million cell updates/sec

Title: US-09-326-285-45
Perfect score: 427
Sequence: 1 atcctcttcggagaagagag.....ggtgtcgcgctgcccccgac 427

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%		Query			DB	ID	Description
Result	No.	Score	Match	Length					
Related	1	427	100.0	3153	4	US-09-080-625-36307123			Sequence 3, Appli
	2	427	100.0	3153	4	US-09-695-782-36433252			Sequence 3, Appli
	3	427	100.0	3336	4	US-09-080-625-2			Sequence 2, Appli
	4	427	100.0	3336	4	US-09-695-782-2			Sequence 2, Appli
	5	427	100.0	3694	4	US-09-080-625-5			Sequence 5, Appli
	6	427	100.0	3694	4	US-09-695-782-5			Sequence 5, Appli
	7	427	100.0	3877	4	US-09-080-625-4			Sequence 4, Appli
	8	427	100.0	3877	4	US-09-695-782-4			Sequence 4, Appli
	9	34.2	8.0	3552	4	US-09-643-597-126			Sequence 126, App
	c 10	34	8.0	1000	4	US-09-641-638-590			Sequence 590, App

1039 bp maize L3 promoter from l301 eosin gene

[

OM nucleic - nucleic search, using sw model

Run on: July 3, 2003, 12:13:11 ; Search time 50.0579 Seconds
 (without alignments)
 7645.798 Million cell updates/sec

Title: US-09-326-285-46
 Perfect score: 1248
 Sequence: 1 cgtgtacaacttggtctctg.....aggcccgactacggccac 1248

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_NA:*
 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	674	54.0	3153	4	US-09-080-625-3	Sequence 3, Appli
2	674	54.0	3153	4	US-09-695-782-3	Sequence 3, Appli
3	674	54.0	3336	4	US-09-080-625-2	Sequence 2, Appli
4	674	54.0	3336	4	US-09-695-782-2	Sequence 2, Appli
5	674	54.0	3694	4	US-09-080-625-5	Sequence 5, Appli
6	674	54.0	3694	4	US-09-695-782-5	Sequence 5, Appli
7	674	54.0	3877	4	US-09-080-625-4	Sequence 4, Appli
8	674	54.0	3877	4	US-09-695-782-4	Sequence 4, Appli
9	177	14.2	1149	4	US-09-257-583-4	Sequence 4, Appli

OM nucleic - nucleic search, using sw model

Run on: July 3, 2003, 12:13:11 ; Search time 33.4923 Seconds
 (without alignments)
 7645.798 Million cell updates/sec

Title: US-09-326-285-47
 Perfect score: 835
 Sequence: 1 atccatatgaagatgtataa.....aggcccgactacggccac 835

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_NA:*
 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	674	80.7	3153	4	US-09-080-625-3	Sequence 3, Appli
2	674	80.7	3153	4	US-09-695-782-3	Sequence 3, Appli
3	674	80.7	3336	4	US-09-080-625-2	Sequence 2, Appli
4	674	80.7	3336	4	US-09-695-782-2	Sequence 2, Appli
5	674	80.7	3694	4	US-09-080-625-5	Sequence 5, Appli
6	674	80.7	3694	4	US-09-695-782-5	Sequence 5, Appli
7	674	80.7	3877	4	US-09-080-625-4	Sequence 4, Appli
8	674	80.7	3877	4	US-09-695-782-4	Sequence 4, Appli

OM nucleic - nucleic search, using sw model

Run on: July 3, 2003, 12:13:11 ; Search time 23.9861 Seconds
 (without alignments)
 7645.798 Million cell updates/sec

Title: US-09-326-285-48
 Perfect score: 598
 Sequence: 1 tgattgactatctcattcct.....aggcccgactacggccac 598

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_NA:*
 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	586	98.0	3153	4	US-09-080-625-3	Sequence 3, Appli
2	586	98.0	3153	4	US-09-695-782-3	Sequence 3, Appli
3	586	98.0	3336	4	US-09-080-625-2	Sequence 2, Appli
4	586	98.0	3336	4	US-09-695-782-2	Sequence 2, Appli
5	586	98.0	3694	4	US-09-080-625-5	Sequence 5, Appli
6	586	98.0	3694	4	US-09-695-782-5	Sequence 5, Appli
7	586	98.0	3877	4	US-09-080-625-4	Sequence 4, Appli
8	586	98.0	3877	4	US-09-695-782-4	Sequence 4, Appli

OM nucleic - nucleic search, using sw model

Run on: July 3, 2003, 12:13:11 ; Search time 10.9101 Seconds
(without alignments)
7645.798 Million cell updates/sec

Title: US-09-326-285-49
Perfect score: 272
Sequence: 1 atcctcttcggagaagagag.....aggcccgactacggccac 272

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	272	100.0	3153	4	US-09-080-625-3	Sequence 3, Appli
2	272	100.0	3153	4	US-09-695-782-3	Sequence 3, Appli
3	272	100.0	3336	4	US-09-080-625-2	Sequence 2, Appli
4	272	100.0	3336	4	US-09-695-782-2	Sequence 2, Appli
5	272	100.0	3694	4	US-09-080-625-5	Sequence 5, Appli
6	272	100.0	3694	4	US-09-695-782-5	Sequence 5, Appli
7	272	100.0	3877	4	US-09-080-625-4	Sequence 4, Appli
8	272	100.0	3877	4	US-09-695-782-4	Sequence 4, Appli

OM nucleic - nucleic search, using sw model

Run on: July 3, 2003, 12:13:11 ; Search time 44.4424 Seconds
(without alignments)
7645.798 Million cell updates/sec

Title: US-09-326-285-38
Perfect score: 1108
Sequence: 1 atccatatgaagatgtataa.....ctcactcgtagtcgtagctc 1108

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	947	85.5	3153	4	US-09-080-625-3	Sequence 3, Appli
2	947	85.5	3153	4	US-09-695-782-3	Sequence 3, Appli

OM nucleic - nucleic search, using sw model

Run on: July 3, 2003, 12:13:11 ; Search time 56.275 Seconds
(without alignments)
7645.798 Million cell updates/sec

Title: US-09-326-285-42
Perfect score: 1403
Sequence: 1 cgtgtacaacttggtctctg.....ggtgtcgcgctgcccccgac 1403

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Match	Length			
1	829	59.1	3153	4	US-09-080-625-3	Sequence 3, Appli
2	829	59.1	3153	4	US-09-695-782-3	Sequence 3, Appli
3	829	59.1	3336	4	US-09-080-625-2	Sequence 2, Appli
4	829	59.1	3336	4	US-09-695-782-2	Sequence 2, Appli
5	829	59.1	3694	4	US-09-080-625-5	Sequence 5, Appli
6	829	59.1	3694	4	US-09-695-782-5	Sequence 5, Appli
7	829	59.1	3877	4	US-09-080-625-4	Sequence 4, Appli
8	829	59.1	3877	4	US-09-695-782-4	Sequence 4, Appli
9	177	12.6	1149	4	US-09-257-583-4	Sequence 4, Appli
c 10	103.8	7.4	4015	4	US-08-810-009-4	Sequence 4, Appli
11	44	3.1	15062	4	US-09-004-838-89	Sequence 89, Appli

OM nucleic - nucleic search, using sw model

Run on: July 3, 2003, 12:13:11 ; Search time 39.7094 Seconds
(without alignments)
7645.798 Million cell updates/sec

Title: US-09-326-285-43
Perfect score: 990
Sequence: 1 atccatatgaagatgtataa.....ggtgtcgcgctgcccccgac 990

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length					
	1	829	83.7	3153	4	US-09-080-625-3			Sequence 3, Appli
	2	829	83.7	3153	4	US-09-695-782-3			Sequence 3, Appli
	3	829	83.7	3336	4	US-09-080-625-2			Sequence 2, Appli
	4	829	83.7	3336	4	US-09-695-782-2			Sequence 2, Appli
	5	829	83.7	3694	4	US-09-080-625-5			Sequence 5, Appli
	6	829	83.7	3694	4	US-09-695-782-5			Sequence 5, Appli
	7	829	83.7	3877	4	US-09-080-625-4			Sequence 4, Appli
	8	829	83.7	3877	4	US-09-695-782-4			Sequence 4, Appli
	9	177	17.9	1149	4	US-09-257-583-4			Sequence 4, Appli
c	10	103.8	10.5	4015	4	US-08-810-009-4			Sequence 4, Appli

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OM nucleic - nucleic search, using sw model

Run on: July 3, 2003, 07:16:56 ; Search time 3094 Seconds
(without alignments)
16837.111 Million cell updates/sec

Title: US-09-326-285-1
Perfect score: 1790
Sequence: 1 cggcctctcccctccctcct.....aaaaaaaaaaaaaaaaaaaaa 1790

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
identical search repeated in GENSEQ, USPATS, USPGPUBS, and EST databases

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 2, 2003, 01:21:21 ; Search time 3432 Seconds
(without alignments)
3324.097 Million cell updates/sec

Title: US-09-326-285-9
Perfect score: 2060
Sequence: 1 MALRLHDVALCLSPPLAARR.....RAKKAGTLPFWSVYGREVQL 392

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US09326285/runat_30062003_121328_8736/app_query.fasta_1.58
3

-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09326285_CGN_1_1_2496@runat_30062003_121328_8736 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*\br/>identical search repeated in GENSEQ, USPATS, USPGPUBS, and EST databases